

SEQUENCE LISTING

Sub A12

(1) GENERAL INFORMATION:

i) APPLICANT: LI, ET AL.

ii) TITLE OF INVENTION: Human Amine Receptor

iii) NUMBER OF SEQUENCES: 8

iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN

(B) STREET: 6 BECKER FARM ROAD

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1

vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: Concurrently

(C) CLASSIFICATION:

vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER:

(B) FILING DATE:

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(viii)

ATTORNEY/AGENT INFORMATION:

(A) NAME: FERRARO, GREGORY D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-

(ix)

TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700
(B) TELEX: 201-994-1744

(2)

INFORMATION FOR SEQ ID NO:1:

(i)

SEQUENCE CHARACTERISTICS

(A) LENGTH: 1380 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii)

MOLECULE TYPE: cDNA

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGAGCTAG CAGGAGTAAC TCTCATGGAA CCTTGGAAAC CATTCTCAA TTGAATTC
GGGCACATTT GAATCAGTAC CCAGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT
CCTCCCTCCTC GTTTCACCCT GTGAGTAATT AACAGACAAA ATTTTTTTTT TTTTTTTTTT
TTTTTTTTTT TTTTGCCCT CCAGTGGAGA AGGTGCCAG TTCTCAGACA GAGGAAGAGT
AGAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT
- Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro

GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT
Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His

ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG
Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met

CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC
Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr

TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC

60

120

180

240

290

338

386

434

482

SUTA12
 Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala
 CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT 530
 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile
 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 578
 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu
 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 626
 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu
 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 674
 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu
 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA 722
 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala
 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT 770
 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp
 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 818
 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val
 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 866
 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe
 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 914
 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
 ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC 962
 Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser
 AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC 1010
 Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr
 CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGG TGG CTG CCC TTC ACC 1058
 Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr
 ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG 1106
 Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu
 GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC 1154
 Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn

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CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA 1202
Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys

CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT 1250
Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp

TTG TAC CAA GAA TGATTCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA 1302
Leu Tyr Gln Glu

CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTG TGGGCATGCT 1362
TCCAGGACAG CATGGGTT 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 337 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro Ala Ala
5 10 15
Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr
20 25 30
Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met
35 40 45
Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser
50 55 60
Tyr Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser
65 70 75
Leu Ala Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu
80 85 90

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Ser	Thr	Ile	Arg	Ser	Val	Glu	Ser	Cys	Trp	Phe	Phe	Gly	Asp	Phe
														105
95														
Leu	Cys	Arg	Ile	His	Thr	Tyr	Leu	Asp	Thr	Leu	Phe	Cys	Leu	Thr
														120
110														
Ser	Ile	Phe	His	Ile	Cys	Phe	Ile	Ser	Ile	Asp	Arg	His	Cys	Ala
														135
125														
Ile	Cys	Asp	Pro	Leu	Leu	Tyr	Pro	Ser	Lys	Phe	Thr	Val	Arg	Val
														150
140														
Ala	Leu	Arg	Tyr	Ile	Leu	Ala	Gly	Trp	Gly	Val	Pro	Ala	Ala	Tyr
														165
155														
Thr	Ser	Leu	Phe	Leu	Tyr	Thr	Asp	Val	Val	Glu	Thr	Arg	Leu	Ser
														180
170														
Gln	Trp	Leu	Glu	Glu	Met	Pro	Cys	Val	Gly	Ser	Cys	Gln	Leu	Leu
														195
185														
Leu	Asn	Lys	Phe	Trp	Gly	Trp	Leu	Asn	Phe	Pro	Leu	Phe	Phe	Val
														210
200														
Pro	Cys	Leu	Ile	Met	Ile	Ser	Leu	Tyr	Val	Lys	Ile	Phe	Val	Val
														225
215														
Ala	Thr	Arg	Gln	Ala	Gln	Gln	Ile	Thr	Thr	Leu	Ser	Lys	Ser	Leu
														240
230														
Ala	Gly	Ala	Ala	Lys	His	Glu	Arg	Lys	Ala	Ala	Lys	Thr	Leu	Gly
														255
245														
Ile	Val	Val	Gly	Ile	Tyr	Leu	Leu	Cys	Trp	Leu	Pro	Phe	Thr	Ile
														270
260														
Asp	Thr	Met	Val	Asp	Ser	Leu	Leu	His	Phe	Ile	Thr	Pro	Pro	Leu
														285
275														
Val	Phe	Asp	Ile	Phe	Ile	Trp	Phe	Ala	Tyr	Phe	Asn	Ser	Ala	Cys
														300
290														
Asn	Pro	Ile	Ile	Tyr	Val	Phe	Ser	Tyr	Gln	Trp	Phe	Arg	Lys	Ala
														315
305														
Leu	Lys	Leu	Thr	Leu	Ser	Gln	Lys	Val	Phe	Ser	Pro	Gln	Thr	Arg
														330
320														
Thr	Val	Asp	Leu	Tyr	Gln	Glu								
335														